

Davenport

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



179/14
Patryk
VED
2000
001/2000

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 08/986,606B

Source: 1653

Date Processed by STIC: 7/11/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 08/986606B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☒ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RECEIVED

JUL 17 2000

TECH CENTER 1000/2900

1653

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/986,606B

DATE: 07/11/2000

TIME: 10:35:46

Input Set : A:\ES.txt

Output Set: N:\CRF3\07112000\H986606B.raw

4 <110> APPLICANT: Sloane, Nathan H
 6 Sixteen Amino Acid of the Antineoplastic Protein (ANUP)
 E--> 6 <112> Sixteen Amino Acid of the Antineoplastic Protein (ANUP)
 7 as a Pharmaceutically Active Anti-Tumor Agent
 W--> 0 <120> TITLE INVENTION:
 W--> 0 <130> FILE REFERENCE:
 9 <140> CURRENT APPLICATION NUMBER: US 08/986,606B
 11 <141> CURRENT FILING DATE: 1997-12-8
 W--> 13 <150> PRIOR APPLICATION NUMBER:
 W--> 15 <151> PRIOR FILING DATE:
 17 <160> NUMBER OF SEQ ID NOS: 1
 20 <170> SOFTWARE: PatentIn ver. 2.0

*IMPORTANT! see item 5
 on Enva
 summary
 sheet*

*Does Not Comply
 Corrected Diskette Needed*

ERRORED SEQUENCES

E--> 23 <210> SEQ ID NO: Seq ID No: #1
 25 <211> LENGTH: 16
 27 <212> TYPE: PRT
 29 <213> ORGANISM: Artificial Sequence
 W--> 31 <220> FEATURE: Xaa is -N-Terminal pyroglutamyl (pyroGLU)
 W--> 33 <221> NAME/KEY:
 35 <222> LOCATION: 1
 37 <223> OTHER INFORMATION: Xaa is pyroGLU
 E--> 39 <400> SEQUENCE: 1
 41 Xaa LEV LYS CYS TYR THR CYS LYS GLU PRO 10
 E--> 42 MET THR SER ALA ALA CYS 16

See next page

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JUL 17 2000

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VERIFICATION SUMMARY

PATENT APPLICATION: US/08/986,606B

DATE: 07/11/2000

TIME: 10:35:47

Input Set : A:\ES.txt

Output Set: N:\CRF3\07112000\H986606B.raw

L:6 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:0 M:201 W: Mandatory field data missing, TITLE INVENTION
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:11 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:13 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:23 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:31 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:39 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
L:42 M:252 E: No. of Seq. differs, <211>LENGTH:Input:16 Found:0 SEQ:0

00/986,606B

TECH. CENTER 10002300

~~SEQUENCE LISTING~~*delete - not used under new Sequence Rules*

<110> Sloane, Nathan H

<112> Sixteen Amino Acid of the Antineoplastic Protein (ANUP)
<120> as a Pharmaceutically Active Anti-Tumor Agent

<140> US 08/986,606

<141> 1997-12-8

<150>

<151>

delete if no response given

<160> 1

<170> PatentIn ver. 2.0

<210> Seq ID No: #1

delete - just use 1

<211> 16

<212> PRT

<213> Artificial Sequence

See Item 12 on Enr Summary Sheet

<220> Xaa is -N-Terminal pyroglutamyl (pyroGLU)

move down - <220> has no

<221>

<222> 1

<223> Xaa is pyroGLU

response. It is a "Leader" only.

<400> 1

Xaa (LEV) LYS CYS TYR THR CYS LYS GLU PRO
MET THR SER ALA ALA CYS10
16*delete - only nucleic acid bases are numbered cumulatively at end of line.**number amino acids under every 5 amino acids. DO NOT use TABS between amino acids. Use space characters*